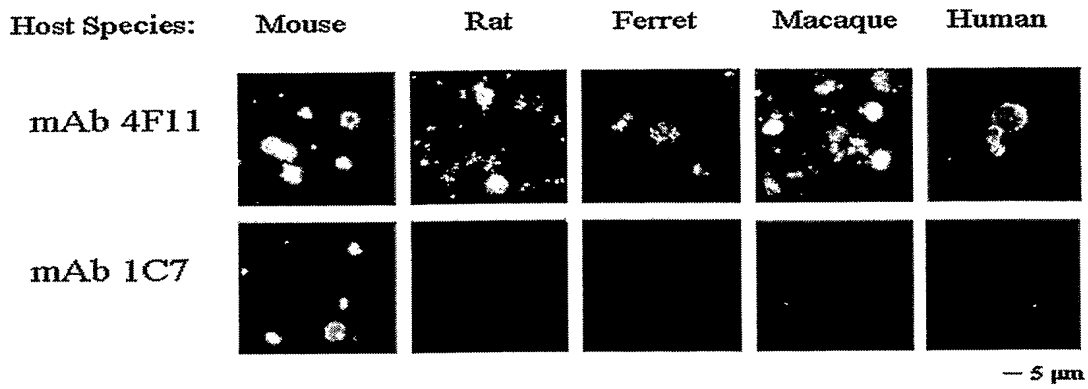


Figure 1

```
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2113 AAACCAACACCTCAACCAACACCTCAGCCAACATCTGAGCCAACATCTGAGCCAACATCTGAGCCAACATCTGAACCAACACCTCAACCAGCACCACCTC
     P  A  P  P  Q  P  A  P  Q  P  A  P  Q  P  A  P  Q  P  A  P  P  Q  P  A  P  P  Q  P  V  P  P  Q  P 768
2213 AACCAGCACCACCTCAACCAGCACCTCAACCAGCACCTCAACCAGCACCTCAACCAGCACCACCTCAACCAGCACCACCTCAACCAGTACCACCTCAACC
     V  P  P  Q  P  M  P  S  R  P  A  P  P  K  P  T  P  Q  P  T  S  E  P  A  P  Q  P  T  S  E  S  T  S  801
2313 AGTACCACCTCAACCAATGCCATCTAGACCAGCACCACCTAAACCAACACCTCAACCAACATCTGAGCCAGCACCTCAACCAACATCTGAGTCAACATCT
     E  P  T  P  R  P  P  P  Q  P  T  S  E  P  T  S  E  P  T  S  E  P  T  S  E  P  S  P  Q  P  T  P  Q  P 835
2413 GAACCAACACCTCGACCACCACCTCAGCCAACATCTGAGCCAACATCTGAACCAACATCTGAACCAACATCTGAACCATCACCTCAACCAACACCTCAAC
     V  P  Q  P  A  P  Q  P  A  P  P  K  P  A  P  K  P  T  P  P  K  P  A  P  K  P  T  P  P  K  P  A  P  868
2513 CAGTACCTCAACCAGCACCTCAACCAGCACCACCTAAACCGGCACCTAAACCAACACCACCTAAACCGGCACCTAAACCAACACCACCTAAACCAGCGCC
     K  P  A  P  S  K  S  S  S  K  P  T  S  T
2613 TAAACCAGCACCATCTAAATCATCATCTAAACCAACATCTACA
```

Figure 2A

```
    T  N  I  S  E  P  A  L  P  D  K  D  P  Q  P  T  S  S  P  Q  P  K  P  R  P  R  P  R  P  Q  P  Q  P  H  34
  1 ACCAATATATCCGAACCAGCACTGCCTGATAAGGATCCTCAACCTACATCTTCACCTCAGCCAAAACCTCGGCCAAGACCTCGACCTCAACCTCAACCTC
    P  H  P  K  P  Q  P  Q  P  T  P  E  P  Q  P  Q  P  A  P  E  P  R  P  Q  P  T  S  K  P  R  P  Q  P  67
101 ATCCACATCCAAAACCTCAGCCTCAGCCGACGCCAGAACCTCAGCCTCAGCCGGCGCCAGAACCTCGACCTCAGCCGACGTCAAAACCTCGACCTCAGCC
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201 AACGTCAAAACCTCGACCTCAGCCGACGCCAGAACCTCGACCTCTGCCGGTGCCAGGACCTGGACCTCTGCCGGTGCCAGGACCTCGACCTCAACCTCAA
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301 CCTCAACCTCAACCTCAGCCTCAACCTCAACCTCAGCCTCAACCTCAACCTCAGCCTCAGCCTCAGCCTCAGCCTCAGCCTCAACCTCAGCCGAAGCCTC
    P  P  S  Q  S  T  S  E  S  A  S  Q  S  K  P  K  P  T  T  Q  T  K  P  S  P  R  P  H  P  K  P  V  P  167
401 AACCACCATCTCAGTCAACATCAGAATCAGCATCGCAATCCAAACCAAAACCAACAACACAAACAAAACCGTCACCGAGACCACACCCAAAGCCGGTGCC
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601 TCTACAAAACCATCTGTGAAACCAACCTCTACAAAGACAACATCAAAACCATCTACAAAACCATCTACAAAACCATCTGTAAAACCAGCCTCTACAAAGA
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701 CAACATCAGAATCAGAAAAACCAACATTGGAAGAAGTTCCAGAAACTAAAGGGAATGGTGTAAGAGTAATAGGATTTGAGGGGTTACAATTATTATCAAT
    I  V  A  I  I  I  G  I  W  I  M  *
801 GATTGTTGCAATAATAATTGGGATATGGATAATGTAAATTTAATTAGAAGTCATTGGCTATTAAATTAATATATAGTAATTTGTAATAATTAGATAAATA

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Figure 2B

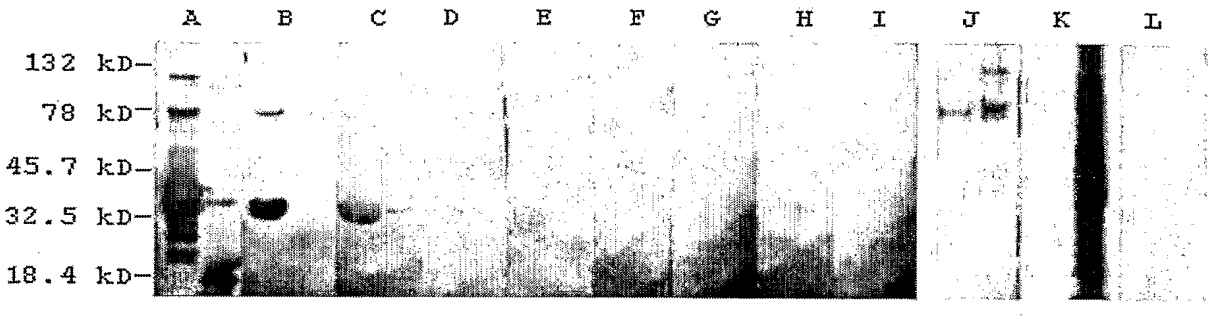
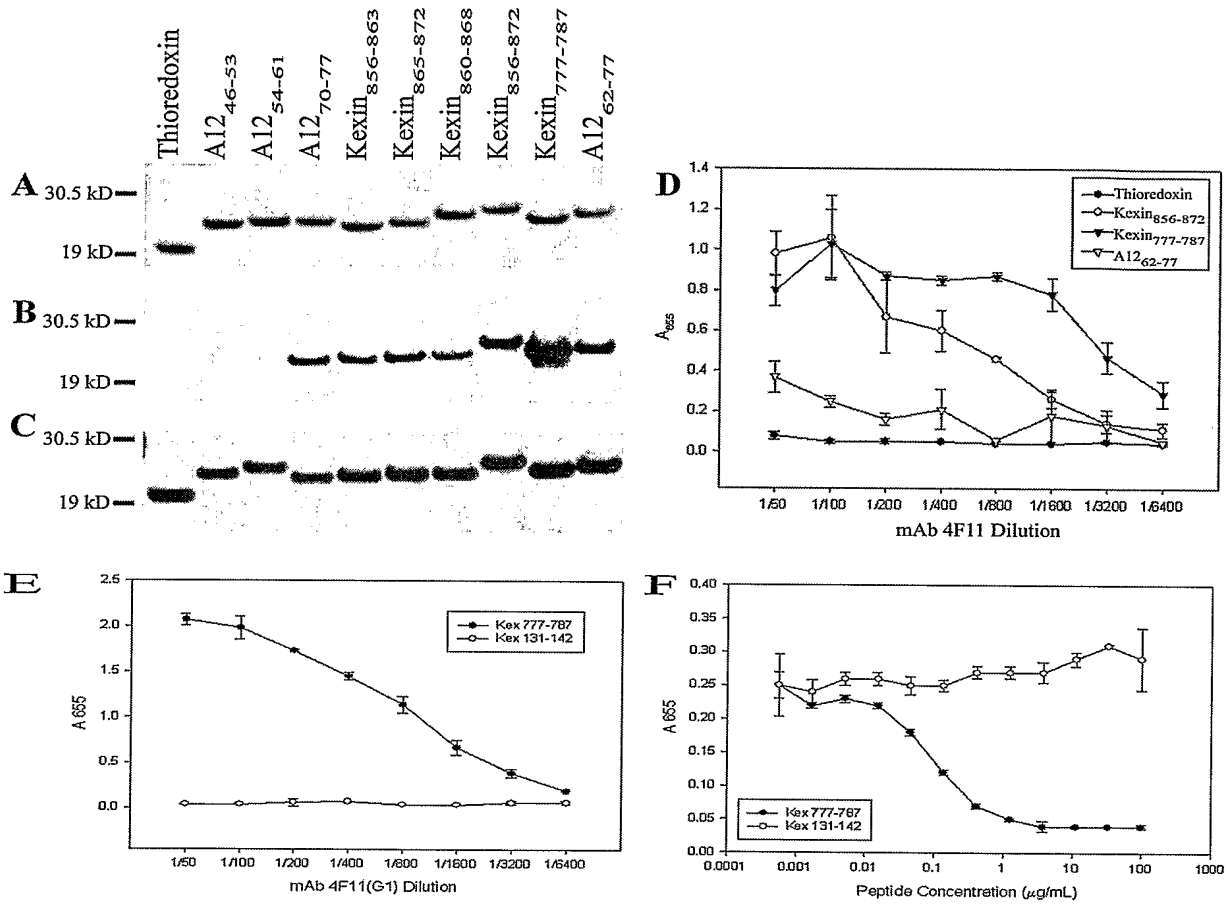



**Figure 3**

| Construct | Sequence of insert |
|---|---|
| $KEXIN_{856-872}$ | KPAPKPTPPKPAPKPAP |
| $KEXIN_{856-863}$ | KPAPKPTP |
| $KEXIN_{865-872}$ | KPAPKPAP |
| $KEXIN_{860-868}$ | KPTPPKPAP |
| $KEXIN_{777-787}$ | RPAPPKPTPQP |
| $A12_{46-53}$ | EPQPQPAP |
| $A12_{54-61}$ | EPRPQPTS |
| $A12_{70-77}$ | KPRPQPTP |
| $A12_{62-77}$ | KPRPQPTS-KPRPQPTP |

**Figure 4**


A
B
C
30.5 kD
19 kD
Thioredoxin
A12 46-53
A12 54-61
A12 70-77
Kexin 856-863
Kexin 865-872
Kexin 860-868
Kexin 856-872
Kexin 777-787
A12 62-77
D
Thioredoxin
Kexin 856-872
Kexin 777-787
A12 62-77
A655
1/50 1/100 1/200 1/400 1/800 1/1600 1/3200 1/6400
mAb 4F11 Dilution
E
Kex 777-787
Kex 131-142
A 655
mAb 4F11(G1) Dilution
F
Kex 777-787
Kex 131-142
A 655
0.0001 0.001 0.01 0.1 1 10 100 1000
Peptide Concentration (μg/mL)

**Figures 5A-F**

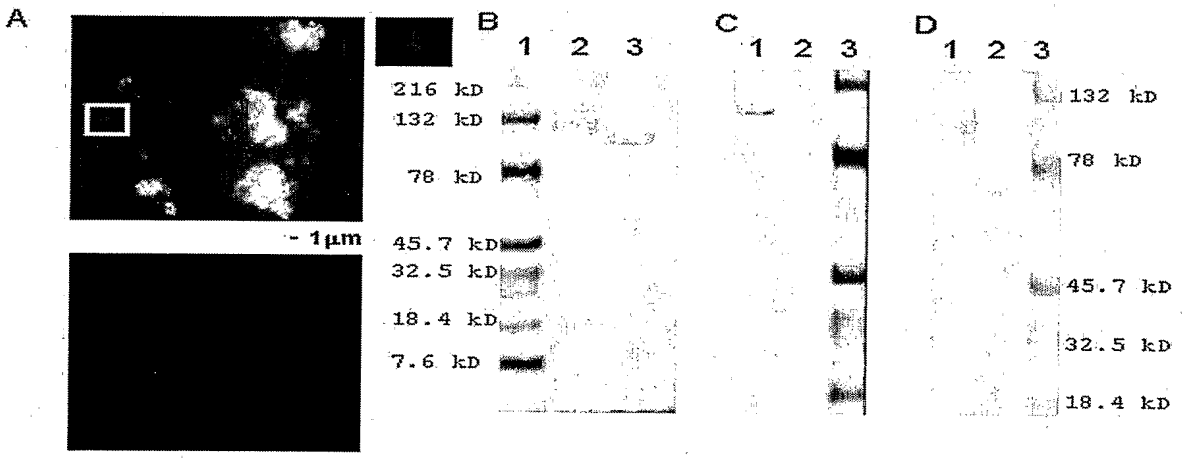
```
URSP2 PspA  EKELKEIDESDSEDYIKEGLRAPLQSKLDAKKAKLSKLEELSDKIDEL   280

URSP2 PspA  DAEIAKLEKDVEDFKNSDGEQAEQYLVAAKKDLDAKKAELENTEADLK   328

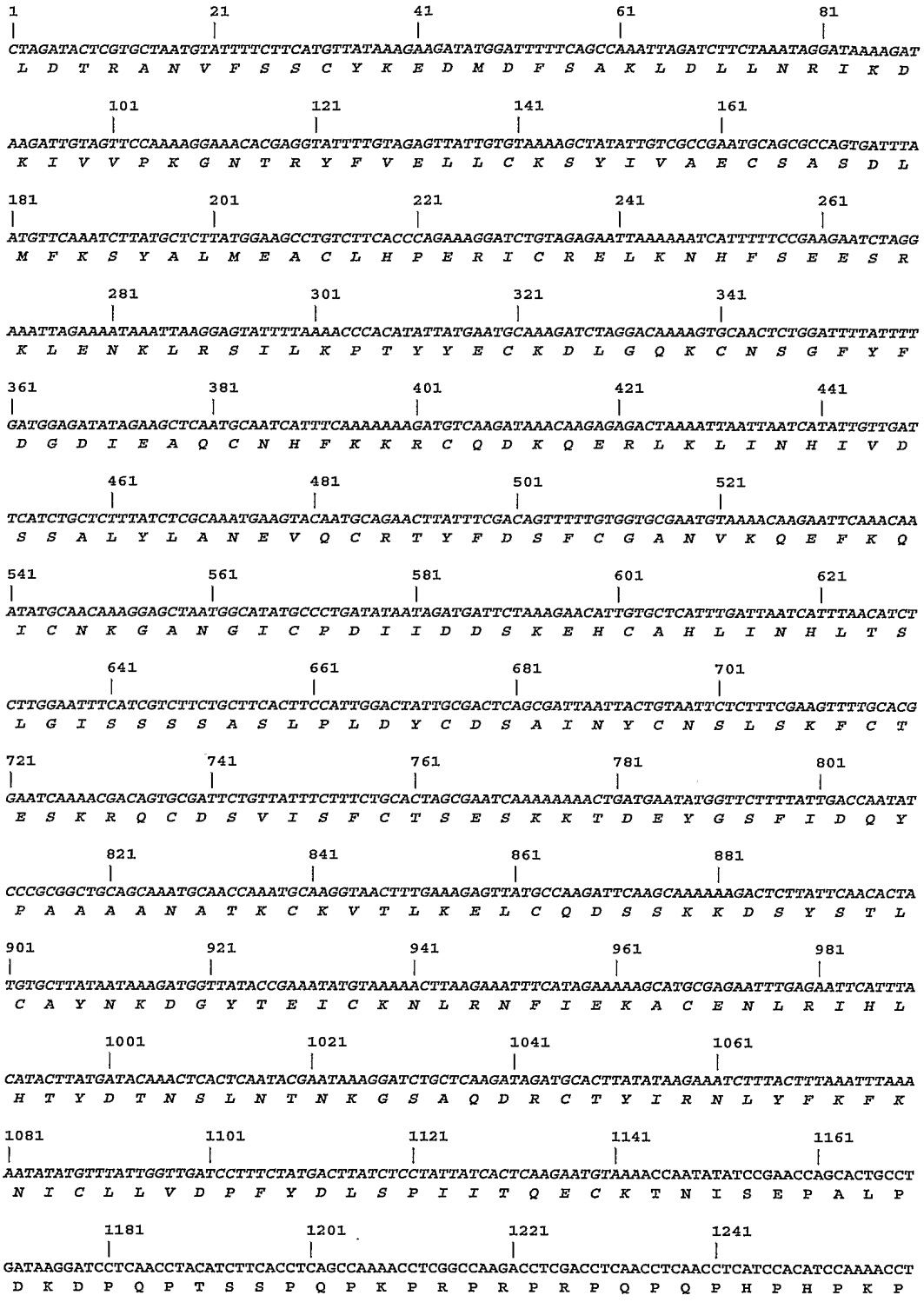
Kex856-872                                  KPAPKPTP.PKPAPKPAP
                                            ||||| | ||||| |||
URSP2 PspA  KAVDEPETPAPAPKPAPAPAPTPEAPAPAPKPAPAPKPAPAPAPTPEA   376
                                              :||| ||| | |
Kex777-787                                    RPAP.PKPTPQP

Kex856-872       KPAPKPTP.PKPAPKPAP
                 ||||| | ||||| |||
URSP2 PspA  PAPAPKPAPAPKPAPAPAPTPEAPAPAPKPAPAPRPAPAPKPAPDPKP   424
                 :||| ||| | |                 |||| ||| | |
Kex777-787       RPAP.PKPTPQP                  RPAP.PKPTPQP
```

**Figure 6**




**Figures 7A-D**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101 121 141 161
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K I V V P K G N T R Y F V E L L C K S Y I V A E C S A S D L
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M F K S Y A L M E A C L H P E R I C R E L K N H F S E E S R
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K L E N K L R S I L K P T Y Y E C K D L G Q K C N S G F Y F
361 381 401 421 441
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D G D I E A Q C N H F K K R C Q D K Q E R L K L I N H I V D
461 481 501 521
TCATCTGCTCTTTATCTCGCAAATGAAGTACAATGCAGAACTTATTTCGACAGTTTTTGTGGTGCGAATGTAAAACAAGAATTCAAACAA
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541 561 581 601 621
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641 661 681 701
CTTGGAATTTCATCGTCTTCTGCTTCACTTCCATTGGACTATTGCGACTCAGCGATTAATTACTGTAATTCTCTTTCGAAGTTTTGCACG
L G I S S S S S A S L P L D Y C D S A I N Y C N S L S K F C T
721 741 761 781 801
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901 921 941 961 981
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N I C L L V D P F Y D L S P I I T Q E C K T N I S E P A L P
1181 1201 1221 1241
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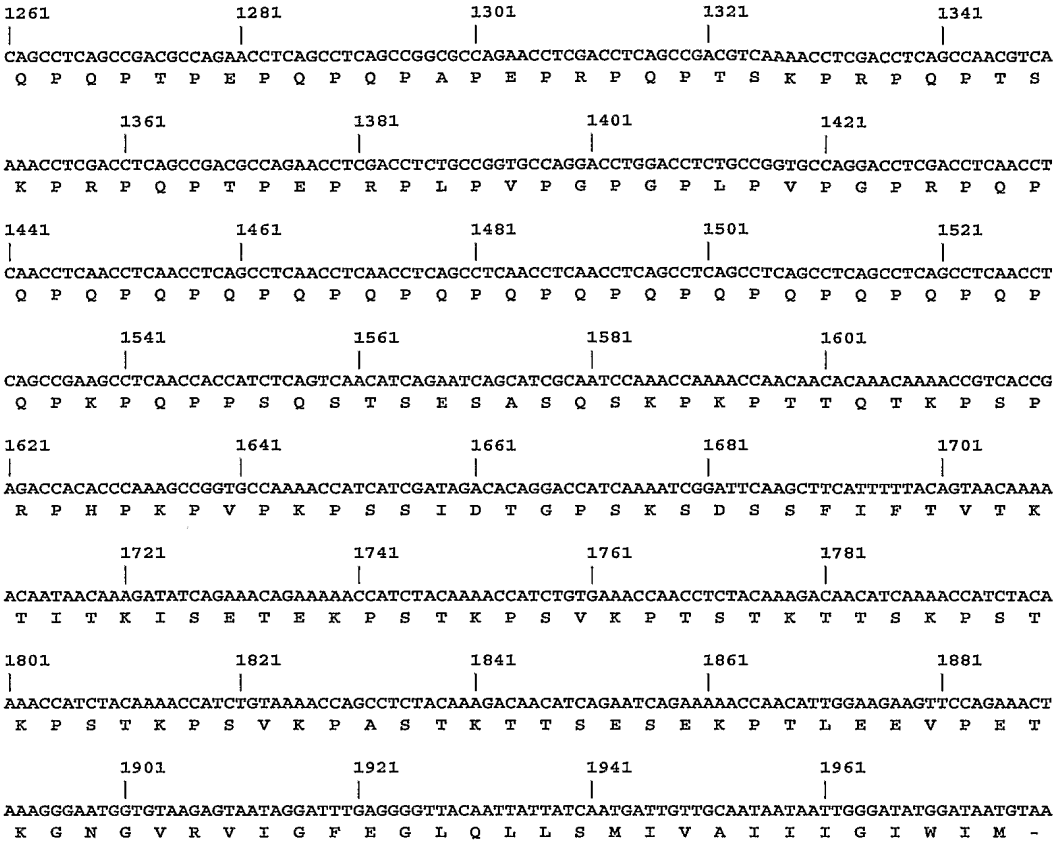
**Figure 8A**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1361 1381 1401 1421
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K P R P Q P T P E P R P L P V P G P G P L P V P G P R P Q P
1441 1461 1481 1501 1521
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1801 1821 1841 1861 1881
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**Figure 8B**